

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 30, 2002, 12:26:53 : Search time 21.3238 Seconds
(without alignments)
2793.134 Million cell updates/sec

Title: US-10-054-680-4
Perfect score: 3228

Sequence: 1 MAMLRQLPPLTSATLHFGLVLT.....ADYGRGCGEDSRDGRASIG 620

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2159.5	66.9	970	2 A36417	Na+/Ca2+-exchangin
2	2147.5	66.5	970	2 S27114	Na+/Ca2+-exchangin
3	2146.5	66.5	973	2 S32815	Na+/Ca2+-exchangin
4	2142.5	66.4	970	2 I48097	Na+/Ca2+-exchangin
5	2138	66.2	957	2 A53789	Na+/Ca2+-exchangin
6	2136.5	66.2	941	2 B53335	Na+/Ca2+-exchangin
7	2135.5	66.2	935	2 S43730	Na+/Ca2+-exchangin
8	2135.5	66.2	958	2 S32435	Na+/Ca2+-exchangin
9	2129.5	66.0	971	2 S28833	Na+/Ca2+-exchangin
10	1954.5	60.5	921	2 A54139	Na+/Ca2+-exchangin
11	1196.5	37.1	890	2 B89047	protein C1068.5 [1
12	633.5	19.6	807	2 T24110	hypothetical prote
13	362.5	11.2	538	2 T00424	probable Na+/Ca2+
14	205	6.4	1014	2 T31433	Na+/Ca2+,K+-exchan
15	198.5	6.1	1199	2 S20969	Na+/Ca2+,K+-exchan
16	187	5.8	4936	2 AH2515	hypothetical prote
17	178.5	5.5	591	2 T19746	hypothetical prote
18	170	5.3	611	2 T21747	hypothetical prote
19	169.5	5.3	3016	2 S77300	hypothetical prote
20	166	5.1	1568	2 T08616	aggregation factor
21	156.5	4.8	2205	2 T08615	aggregation factor
22	150.5	4.7	591	2 S40705	Na+/Ca2+,K+-exchan
23	144.5	4.5	703	2 T03888	Na+/Ca2+,K+-exchan
24	144	4.5	644	2 B96582	hypothetical prote
25	144	4.5	1428	2 AC2224	hypothetical prote
26	132	4.1	1807	2 JC6319	integrin beta-4 ch
27	131.5	4.1	826	2 AB1841	hypothetical prote
28	131	4.1	590	2 S40707	hypothetical prote
29	126.5	3.9	1875	2 A36429	integrin beta-4 ch

30	126	3.9	4199	2 S76412	hypothetical prote
31	124	3.8	318	2 A83708	hypothetical prote
32	122	3.8	825	2 T08617	aggregation factor
33	121.5	3.8	651	2 T03889	Na+/Ca2+,K+-exchan
34	121.5	3.8	743	2 T38674	probable membrane
35	119.5	3.7	433	2 S74922	hypothetical prote
36	119	3.7	3972	2 S75251	hypothetical prote
37	115	3.6	324	2 A10434	probable sodium/ca
38	114	3.5	1748	2 JN0786	integrin beta-4 ch
39	113	3.5	332	2 H82064	conserved hypothet
40	112.5	3.5	375	2 I40554	rap60 protein - Ba
41	110	3.4	2397	2 A55535	versican precursor
42	109	3.4	769	2 G95270	hypothetical prote
43	108.5	3.4	652	2 A37000	leukemia virus rec
44	108	3.3	673	2 VCPV85	coat protein vp1 -
45	107.5	3.3	1263	2 T00649	hypothetical prote

ALIGNMENTS

RESULT 1

A36417 Na+/Ca2+-exchanging protein - dog

C:Species: Canis lupus familiaris (dog)

C>Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 18-Aug-2000

C:Accession: A36417

R:Nicolli, D.A.; Longoni, S.; Philipson, K.D.

Science 250, 562-565, 1990

A:Title: Molecular cloning and functional expression of the cardiac sarcolemmal Na(+)

A:Reference number: A36417; MUID:91047958; PMID:11700476

A:Accession: A36417

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-970 <NIC>

A:Cross-references: GB:M57523; NID:g164072; PID:AAA62766.1; PID:g164073; GB:M36119

C:Superfamily: human Na+/Ca2+-exchanging protein

C:Keywords: phosphoprotein; transmembrane protein

Query Match	66.9%	Score 2159.5	DB 2	Length 970
Best Local Similarity	69.9%	Pred. No. 2.9e-157		
Matches 425	Conservative 73	Mismatches 89	Indels 21	Gaps 8
QY	1	MAMLRQLPPLTSATLHFGLVLT--LNGLRABAGSGDVPSTQNNESGSSDCEGV	58	
DB	1	MLQRLPLTFSGCHLLAVVALLFSDHDLISATFEMEGNETGE---CTGSYCKKGV	56	
QY	59	ILPIWYEPNPSLGDKIARVIVFYVALIYMFGLVSIIDRFMASTLEVITSOREVTIKKPN	118	
DB	57	ILPIWEPDPSFGDKINARVIVFYVALIYMFGLVSIIDRFMASTLEVITSOREVTIKKPN	116	
QY	119	GETSTTIRVWNETVSNLTALGSSAPEILLSTIEVCGHGFGLDLPSTIVGSAFNM	178	
DB	117	GETTKTVIRVWNETVSNLTALGSSAPEILLSTIEVCGHGFGLDLPSTIVGSAFNM	176	
QY	179	FIITGICVYVLPDETRIKRLRVFTTAASTFATVITLVITLAVSPGCVQVREGILTL	238	
DB	177	FIITALCVYVLPDETRIKRLRVFTTAASTFATVITLVITLAVSPGCVQVREGILTL	236	
QY	239	FEFVPCVLLAVNADKRLLEFYMKKRYRTDKHGIITTEGDHKG--IPMDKMMNSH	295	
DB	237	FEFVICVYVAVNADKRLLEFYMKKRYRTDKHGIITTEGDHKG--IPMDKMMNSH	296	
QY	296	--FLDGNLVPLEGEVD---ESRREMIRILDKOKHPEKDDQLEVAMANYALSHQ	348	
DB	297	VDFNLGALV--LEVDERDQDEDEARREMARILKELKQHPKEIQELIANVQVLSQO	355	
QY	349	KSRAPFYRIQATRMATGAGNITIKKAAEADAKASSMEVNHDEPE--DPISKYFPQCSYOC	407	
DB	356	KSRAPFYRIQATRMATGAGNITIKKAAEADAKASSMEVNHDEPE--DPISKYFPQCSYOC	415	
QY	408	LENGAVLLTVVRKGDMSTKVYDYKTEDGSANAAGADYEFTGCTVYVLPQETQKERSVG	467	

Db 416 LENCVALTLTIIRGCDLTNTVFVDFRTEDGTNAGSDVEFTEGTVFKFGFQKRIKRG 475

Qy 468 IIDDIFEEDEHFEVRLSNVRIEEQPEEGMPAIFNSLPLPRAVLASPCVATVITLDD 527

Db 476 IIDDIFEEDEENFLVHLSNVKVSSEASDEGLIENHVS---ALACLGSPSTAVTTFDD 532

Qy 528 HAGIFFECDTIVHVSISIGIMEYKVLRTSGARCTVYPPRTVEGTAKGGGEDEEDTIGEL 567

Db 533 HAGIFFECDTIVHVSISIGIMEYKVLRTSGARCNVYIPYKTIGTARGGGEDEEDTIGEL 592

Qy 588 EFKNDETV 595

Db 593 EFNDETV 600

RESULT 2

S27114

Na+/Ca2+-exchanging protein precursor, cardiac - bovine

N:Alternate names: Na+/Ca2+ antiporter

C:Species: Bos primigenius taurus (cattle)

C:Date: 22-Nov-1993 #sequence_revision 23-Mar-1995 #text_change 18-Aug-2000

A:Accession: S27114; S18388

Aceto, J.F.; Condrescu, M.; Kriopis, C.; Nelson, H.; Nelson, N.; Nicoll, D.; Philipson

Arch. Biochem. Biophys. 298, 553-560, 1992

A:Title: Cloning and expression of the bovine cardiac sodium-calcium exchanger.

A:Reference number: S27114; MUID:93037494; PMID:1416984

A:Accession: S27114

A:Molecule type: mRNA

A:Residues: 1-970 <ACE>

A:Cross-references: GB:U06438; NID:9163033; PIDN:AAA0509.1; PID:9163034

R:Burkin, J.T.; Ahrens, D.C.; Pan, J.C.E.; Reeves, J.P.

Arch. Biochem. Biophys. 290, 369-375, 1991

A:Title: Purification and amino-terminal sequence of the bovine cardiac sodium-calcium exchanger.

A:Reference number: S18388; MUID:92027750; PMID:1929404

A:Accession: S18388

A:Molecule type: protein

A:Residues: 33-40, 'X', 42-44 <DUR>

A:Experimental source: heart

C:Superfamily: human Na+/Ca2+-exchanging protein

C:Keywords: cardiac muscle; heart; ion transport; membrane protein

F:1-33/Domain: signal sequence <status predicted <SIG>

F:33-970/Product: Na+/Ca2+ exchange protein, cardiac #status predicted <MAT>

Query Match 66.5%; Score 2147.5; DB 2; Length 970;

Best Local Similarity 69.4%; Pred. No. 2,4e-156;

Matches 422; Conservative 74; Mismatches 91; Indels 21; Gaps 8;

Qy 1 MAMLRLOPLTSNLFHGLTVFLF--LNGLRAGAGSGDVPSTGONNESCSSGSDCKEYV 58

1 MLOFSLSPFLSMGFHIAVVALLESHVDHISATETMEGEGNETGE---CTGSYCKKGV 56

Qy 59 ILPIWYENPDSLGDKIARIVYFVALIYMFGLVSIADRFMAISIEVITSQEREVTIKKPN 118

57 ILPIWYENPDSLGDKIARIVYFVALIYMFGLVSIADRFMAISIEVITSQEREVTIKKPN 116

Qy 119 GETSTTTIRVWNETVSNLTLMALGSSAPETLSLIEVCGHGFIAGDLGPTTVGSAAFNM 178

117 GETTTTVIRWNETVSNLTLMALGSSAPETLSLIEVCGHGFIAGDLGPTTVGSAAFNM 176

Qy 179 FTITIGCVYVDPDGETRKIKHLRVFFITPAASIFAYIMLYMLAIVPSGVVOYWGGLTL 238

177 FTITIGCVYVDPDGETRKIKHLRVFFITPAASIFAYIMLYMLAIVPSGVVOYWGGLTL 236

Qy 239 FFFPVCVLLAAVADRRLLEFYKMHKKYRTDKRGITIEEGDHPK---IENDGKMMNSH 295

237 FFFPVCVLLAAVADRRLLEFYKMHKKYRTDKRGITIEEGDHPK---IENDGKMMNSH 296

Qy 296 ---FLDGNLVPLEGEVD---ESRREMTIRLDKOKHPEKDLQVEMANYVALSHOO 348

297 VDSFLDGNLVPLEGEVD---ESRREMTIRLDKOKHPEKDLQVEMANYVALSHOO 355

Qy 349 KSRAPYRIQATRLMTAGNILKHAADQARKAVSMHEVNTVAENDPVSKIEFGDTYOC 407

Db 356 KSRAPYRIQATRLMTAGNILKHAADQARKAVSMHEVNTVAENDPVSKIEFGDTYOC 415

Qy 408 LENCVALTLTVVARGGDMKTMVDYKTEDGSANACADYEFTEGTVLKPGEQKESYVG 467

Db 416 LENCVALTLTIIRGCDLTNTVFVDFRTEDGTNAGSDVEFTEGTVFKFGFQKRIKRG 475

Qy 468 IIDDIFEEDEHFEVRLSNVRIEEQPEEGMPAIFNSLPLPRAVLASPCVATVITLDD 527

Db 476 IIDDIFEEDEENFLVHLSNVKVSLEASDEGLIENHVS---TLACLGSPSTAVTTFDD 532

Qy 528 HAGIFFECDTIVHVSISIGIMEYKVLRTSGARCTVYPPRTVEGTAKGGGEDEEDTIGEL 567

Db 533 HAGIFFECDTIVHVSISIGIMEYKVLRTSGARCNVYIPYKTIGTARGGGEDEEDTIGEL 592

Qy 588 EFKNDETV 595

Db 593 EFNDETV 600

RESULT 3

S32815

Na+/Ca2+-exchanging protein - human

N:Alternate names: Na+/Ca2+ antiporter; Na+/Ca2+ exchanger

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Nov-2000

A:Accession: S32815; A56767

R:Komuro, I.; Wenninger, K.E.; Philipson, K.D.; Izumo, S.

Proc. Natl. Acad. Sci. U.S.A. 89, 4769-4773, 1992

A:Title: Molecular cloning and characterization of the human cardiac Na(+)/Ca(2+) exc

A:Reference number: S32815; MUID:92262521; PMID:1374913

A:Accession: S32815

A:Molecule type: preliminary

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-973 <IZU>

A:Cross-references: EMBL:M91368; NID:9180672; PIDN:AAA35702.1; PID:9180673

R:Kotuji, P.; Hadley, R.W.; Kieval, R.S.; Lederer, W.J.; Schulze, D.H.

Am. J. Physiol. 263, C1241-C1249, 1992

A:Title: Expression of the Na-Ca exchanger in diverse tissues: a study using the clon

A:Reference number: A56767; MUID:93118744; PMID:1476165

A:Accession: A56767

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 4-253, 'K', 255-627, 'K', 629-692, 'K', 694-973 <KOF>

A:Note: sequence extracted from NCBI backbone (NCBIN:121726, NCBI:P:121727)

C:Superfamily: human Na+/Ca2+-exchanging protein

C:Keywords: cardiac muscle; heart; phosphoprotein; transmembrane protein

Query Match 66.5%; Score 2146.5; DB 2; Length 973;

Best Local Similarity 69.2%; Pred. No. 2.9e-156;

Matches 421; Conservative 76; Mismatches 90; Indels 21; Gaps 8;

Qy 1 MAMLRLOPLTSNLFHGLTVFLF--LNGLRAGAGSGDVPSTGONNESCSSGSDCKEYV 58

4 MRLSLSPFLSMGFHILVLSLFSHVDHVAIETMEGEGNETGE---CTGSYCKKGV 59

Qy 59 ILPIWYENPDSLGDKIARIVYFVALIYMFGLVSIADRFMAISIEVITSQEREVTIKKPN 118

60 ILPIWYENPDSLGDKIARIVYFVALIYMFGLVSIADRFMAISIEVITSQEREVTIKKPN 119

Qy 119 GETSTTTIRVWNETVSNLTLMALGSSAPETLSLIEVCGHGFIAGDLGPTTVGSAAFNM 178

120 GETTTTVIRWNETVSNLTLMALGSSAPETLSLIEVCGHGFIAGDLGPTTVGSAAFNM 179

Qy 179 FTITIGCVYVDPDGETRKIKHLRVFFITPAASIFAYIMLYMLAIVPSGVVOYWGGLTL 238

180 FTITIGCVYVDPDGETRKIKHLRVFFITPAASIFAYIMLYMLAIVPSGVVOYWGGLTL 239

Qy 239 FFFPVCVLLAAVADRRLLEFYKMHKKYRTDKRGITIEEGDHPK---IENDGKMMNSH 295

240 FFFPVCVLLAAVADRRLLEFYKMHKKYRTDKRGITIEEGDHPK---IENDGKMMNSH 299

Qy 296 ---FLDGNLVPLEGEVD---ESRREMTIRLDKOKHPEKDLQVEMANYVALSHOO 348

```
Db 300 VENFDGALV-LEVDERDODDEAREMARILKELKOKHPKEIRBOLIELANYQVLSQQ 358
Oy 349 KSRATYRQATRTMTGAGNIILKHAADQAKKASSSEVHTDPE-DFISKVFFDPCSTQC 407
Db 359 KSRATYRQATRTMTGAGNIILKHAADQAKKASSSEVHTDPE-DFISKVFFDPCSTQC 418
Oy 408 LENCAGVLTIVRKGDMSKTYVDYKTEDGSANAGADYEFTGTVVILKPGETOKEFSYG 467
Db 419 LENCSTVALTIIRRGDGLTNVYFVDFRTEDGTANAGSDYEFTGTVVIRKPGETOKEIRYG 478
Oy 468 IIDDIFEEDEHFVRLSNVRIEEOPEGMIPAIFNSLPRAVLASPCVATVITLDD 527
Db 479 IIDDIFEEDEHFVRLSNVKSSEASEDGLLEANHVS---TLACLGSPSTATVITFD 535
Oy 528 HAGITFEEDCDTHVSESGVMEVKLRTSGANGTYIYPRVYEGTAKGGEFEDTGYEL 587
Db 536 HAGITFEEDPYTHVSESGIMEVKLRTSGANGNIVPYKITEGTARGGEDFEDTCGL 595
Y 588 EFKNDETV 595
Db 596 EFQNDIEIV 603

RESULT 4
148097
Na+/Ca2+-exchanging protein - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Aug-2000
C:Accession: 148097
R:Tauruys, Y.; Bersohn, M.M.; Li, Z.; Nicoll, D.A.; Philipson, K.D.
A:Title: Molecular cloning and functional expression of the guinea pig cardiac Na(+)-Ca2+
A:Reference number: 148097; MUID:95076257; PMID:7968617
A:Accession: 148097
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-970 <RES>
A:Cross-references: EMBL:U04955; NID:9927230; PIDN:AA73904.1; PID:9507350
C:Superfamily: human Na+/Ca2+-exchanging protein

Query Match 66.4%; Score 2142.5; DB 2; Length 970;
Best Local Similarity 69.1%; Pred. No. 5.8e-156;
Matches 420; Conservative 76; Mismatches 91; Indels 21; Gaps 9;

Oy 1 MAMRLQOLTSALFLH-FLGLVTFVL-FLNGLRARAGSGDVPSTGQNNESGSSGCKB 58
Db 1 MURLSLPTYSGLGFLHLLAMTLLISHVDHTAET---EMVEEGNETGECTGTSYCKRGV 56
Oy 59 ILPIWYPPNPISGLDKIARIVYFVALIYMFGLGVSIIADRFMASIEVITSQREVTIKRPN 118
Db 57 ILPIWEPDPSFGDKIARATYFVAMVYMFGLGVSIIADRFMSIEVITSQREVTIKRPN 116
Oy 119 GETSTTTRVWNETVSNLTLMALGSSAPRILLSLIEVCGHGFIAGDLGPSTTVGSAAFNM 178
Db 117 GETTKTYRINWNETVSNLTLMALGSSAPRILLSLIEVCGHGNETAGDLGPSTTVGSAAFNM 176
Oy 179 FLIIGICVYVVPDGETRRIKHLRVFFITPAWSIFAYIWLMLAYLAFSPGVQVWVGSLTL 238
Db 177 FLIILALCYVVPDGETRRIKHLRVFFITPAWSIFAYIWLMLAYLAFSPGVQVWVGSLTL 236
Oy 239 FFFPVCVLAVADKRLLEFYKMKHKYRTDKRGIIETEGDHPG---IENDGKMMNSH 295
Db 237 FFFPVCVFAVWADKRLLEFYKMKHKYRTDKRGIIETEGDHPG---IENDGKMMNSH 296
Oy 296 ---FLDGLNVLPLEGEVD---ESRREMIRILKDKOKHPKEDLDQVLEMANVYALS HQ 348
Db 297 VENFDGALV-LEVDERDODDEAREMARILKELKOKHPKEIRBOLIELANYQVLSQQ 355
Oy 349 KSRATYRQATRTMTGAGNIILKHAADQAKKASSSEVHTDPE-DFISKVFFDPCSTQC 407
Db 356 KSRATYRQATRTMTGAGNIILKHAADQAKKASSSEVHTDPE-DFISKVFFDPCSTQC 415
Oy 408 LENCAGVLTIVRKGDMSKTYVDYKTEDGSANAGADYEFTGTVVILKPGETOKEFSYG 467
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```
Db 416 LENCSTVALTIIRRGDGLTNVYFVDFRTEDGTANAGSDYEFTGTVVIRKPGETOKEIRYG 475
Oy 468 IIDDIFEEDEHFVRLSNVRIEEOPEGMIPAIFNSLPRAVLASPCVATVITLDD 527
Db 476 IIDDIFEEDEHFVRLSNVKSSEASEDGLLEANHVS---TLACLGSPSTATVITFD 532
Oy 528 HAGITFEEDCDTHVSESGVMEVKLRTSGANGTYIYPRVYEGTAKGGEFEDTGYEL 587
Db 533 HAGITFEEDPYTHVSESGIMEVKLRTSGANGNIVPYKITEGTARGGEDFEDTCGL 592
Oy 588 EFKNDETV 595
Db 593 EFQNDIEIV 600

RESULT 5
A53769
Na+/Ca2+-exchanging protein precursor, splice form NACA7 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 18-Aug-2000
C:Accession: A53769; JX0288
R:Lee, S.L.; Yu, A.S.L.; Lytton, J.
J. Biol. Chem. 269, 14849-14852, 1994
A:Title: Tissue-specific expression of Na(+)-Ca(2+) exchanger isoforms.
A:Reference number: A53769; MUID:94253030; PMID:8195112
A:Accession: A53769
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-957 <LE>
A:Cross-references: GB:U04933; NID:9451571; PIDN:AB39952.1; PID:9451572
R:Nakasaki, Y.; Yamoto, T.; Hanada, H.; Imagawa, T.; Shigekawa, M.
J. Biochem. 114, 528-534, 1993
A:Title: Cloning of the rat aortic smooth muscle Na+/Ca2+ exchanger and tissue-specific
A:Reference number: JX0288; MUID:94103175; PMID:8276763
A:Accession: JX0288
A:Molecule type: mRNA
A:Residues: 1-957 <NAK>
A:Experimental source: aortic smooth muscle
A:Superfamily: human Na+/Ca2+-exchanging protein
C:Keywords: ion transport; membrane protein
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-957/Product: Na+/Ca2+ exchanger #status predicted <MAT>

Query Match 66.2%; Score 2138; DB 2; Length 957;
Best Local Similarity 67.9%; Pred. No. 1.3e-155;
Matches 424; Conservative 73; Mismatches 87; Indels 40; Gaps 10;

Oy 4 LRLQOLTSALFLHFGVTFVFL-----NGLRABAGSGDVPSTGQNNESGSSGCK 55
Db 2 LRLSLPPNWSKGRFLVTLVALLFTVHDHTADTEATGQ-----ETTECTGTSYCK 53
Oy 56 EGVILPIWYPPNPISGLDKIARIVYFVALIYMFGLGVSIIADRFMASIEVITSQREVTIK 115
Db 54 KGVILPIWEPDPSFGDKIARATYFVAMVYMFGLGVSIIADRFMSIEVITSQREVTIK 113
Oy 116 KPNGETSTTTRVWNETVSNLTLMALGSSAPRILLSLIEVCGHGFIAGDLGPSTTVGSA 175
Db 114 KPNGETSTTTRVWNETVSNLTLMALGSSAPRILLSLIEVCGHGNETAGDLGPSTTVGSA 173
Oy 176 FFMFLIIGICVYVVPDGETRRIKHLRVFFITPAWSIFAYIWLMLAYLAFSPGVQVWVGSL 235
Db 174 FFMFLIILALCYVVPDGETRRIKHLRVFFITPAWSIFAYIWLMLAYLAFSPGVQVWVGSL 233
Oy 236 LTLFFPVCVLAVADKRLLEFYKMKHKYRTDKRGIIETEGDHPG---IENDGKMM 292
Db 234 LTLFFPVCVFAVWADKRLLEFYKMKHKYRTDKRGIIETEGDHPG---IENDGKMM 293
Oy 293 NSH---FLDGLNVLPLEGEVD---ESRREMIRILKDKOKHPKEDLDQVLEMANVYALS 345
Db 294 NSHWNFDGALV-LEVDERDODDEAREMARILKELKOKHPKEIRBOLIELANYQVLS 352
Oy 346 HOKSRATYRQATRTMTGAGNIILKHAADQAKKASSSEVHTDPE-DFISKVFFDPC 404
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```
|||||
Db 353 QOQKSRAFRIQATRLMTGNTLKRAADQARKAVSMHVNMDVVENDPVSFFEQGT 412
405 YQLENCQAVLTVVRKGGMSKTMVVDYKTEKDSANAGADYFETGTVLTKGGEPOKE 464
413 YQLENCQAVLTVVRKGGMSKTMVVDYKTEKDSANAGADYFETGTVLTKGGEPOKE 472
465 SVGIIDDDIFEEDHFFVRLSNVRIEEOPEEGMPAIFNSLPUR-AVLASPCVATVTI 523
473 RVGIIDDDIFEEDHFFVRLSNVRIEEOPEEGMPAIFNSLPUR-AVLASPCVATVTI 528
Qy 524 LDDDHAGIFTEECDDTHVSSISGVMEYKVLRTSGARCTVVPRTVEGTAKGGEDFET 583
Db 529 FDDDHAGIFTEECDDTHVSSISGVMEYKVLRTSGARCTVVPRTVEGTAKGGEDFET 588
Qy 584 YGELEFRKNDTV-----CDROE 600
Db 589 CGELEFRKNDTV-----CDROE 612
```

RESULT 6

53335

+/Ca2+-exchanging protein NCX1, splice form NACA6 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 18-Aug-2000

C:Accession: B53335

R:Kofuji, P.; Lederer, W.J.; Schulze, D.H.

J. Biol. Chem. 269, 5145-5149, 1994

A:Title: Mutually exclusive and cassette exons underlie alternatively spliced isoforms

A:Reference number: A53335; MID:94148976; PMID:8106495

A:Accession: B53335

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-941 <KOF>

A:Experimental source: brain

A:Note: sequence extracted from NCBI backbone (NCBI:144050)

C:Superfamily: human Na+/Ca2+-exchanging protein

Query Match 66.2%; Score 2136.5; DB 2; Length 941;

Best Local Similarity 69.5%; Pred. No. 1.6e-155;

Matches 417; Conservative 76; Mismatches 86; Indels 21; Gaps 9;

```
Qy 8 PLTSAPLHGLVTFVFL-LNGLRAGSGDVPSTGQNNESGSSDCKEGLVLPITYPE 66
Db 9 PFMGCFILALVALFEFRVDHVSATMEEGENETGE---CTGSYYCKGVLPIWEPQ 64
Qy 67 NPSLGDKIARIVYFVALIYMLGVSIIADRPMASTEVITSOERETIKKPNGETSTTI 126
Db 65 DPSFGDIARATVYFVAMVYMLGVSIIADRPMSIEVITSOERETIKKPNGETSTTI 123
127 RVNNETVSNLTLMALGSSAPEILSLIEVCGHGFAGDLGPTIVGSAFNMFLIIGCV 186
Db 124 RINNETVSNLTLMALGSSAPEILSLIEVCGHGFAGDLGPTIVGSAFNMFLIIGCV 183
Qy 187 YVIPDETTRIKILRVFFITTAANSIFAYITWYILAVSPGVQVWEGLLTFFPVCYL 246
Db 184 YVVPDETTRIKILRVFFITTAANSIFAYITWYILAVSPGVQVWEGLLTFFPVCYL 243
Qy 247 LAAVAAKRLLEFYKMHKKYKTDKNGIITTEEDHPK---TEMCKMNMHSH---FLDGN 300
Db 244 EAAVAAKRLLEFYKMHKKYKTDKNGIITTEEDHPK---TEMCKMNMHSH---FLDGN 303
Qy 301 LVPLEGEKVD---ESRREMIIRILDKOKHPEKDLQVLEMANUYALSHQKSRAFYRI 356
Db 304 LV-LVDERQDDEARREARILKELKOKHPEKDLQVLEMANUYALSHQKSRAFYRI 362
Qy 357 QATRTMTAGNIIILKHAADQARKAVSMHVNMDVVENDPVSFFEQGT 412
Db 363 QATRTMTAGNIIILKHAADQARKAVSMHVNMDVVENDPVSFFEQGT 422
Qy 416 LTVVRKGGMSKTMVVDYKTEKDSANAGADYFETGTVLTKGGEPOKE 475
Db 423 LTVVRKGGMSKTMVVDYKTEKDSANAGADYFETGTVLTKGGEPOKE 482
```

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Qy 476 EDEHFEVRLSNVRIEEOPEEGMPAIFNSLPUR-RAVLASPCVATVTI 535
Db 483 EDENFLVHLNSVAVSSBTSBDGLLEANNHS---TLACLSGPTATVATVFDHAGJFTFE 539
Qy 536 CDTHVSESGIEMEVKVLRTSGARCTVVPRTVEGTAKGGEDFETGGELEFRKNDTV 595
Db 540 ESVTHVSESGIEMEVKVLRTSGARCTVVPRTVEGTAKGGEDFETGGELEFRKNDTV 599
```

RESULT 7

543730

Na+/Ca2+-exchanging protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 18-Aug-2000

C:Accession: S43730

R:Purman, I.; Cook, O.; Kasir, J.; Rahamimoff, H.

FEBS Lett. 319, 105-109, 1993

A:Title: Cloning of two isoforms of the rat brain Na(+-)Ca(2+) exchanger gene and the

A:Reference number: S32435; MID:93202244; PMID:8454039

A:Accession: S43730

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-935 <RUP>

A:Cross-references: EMBL:X68812; NID:g288229; PIDN:CAA48707.1; PID:g288230

C:Superfamily: human Na+/Ca2+-exchanging protein

Query Match 66.2%; Score 2135.5; DB 2; Length 935;

Best Local Similarity 68.8%; Pred. No. 1.9e-155;

Matches 421; Conservative 72; Mismatches 86; Indels 33; Gaps 9;

```
Qy 4 LRLQPLTSAPLHGLVTFVFL-----NLGRAAGSGDVPSTGQNNESGSSDCK 55
Db 2 LRLSLPNTSMGFRLLVALFTVHDHITADFEAENGQ-----ETTECTGSYYCK 53
Qy 56 EGYILPWPENSLGDKTARVYFVALIYMLGVSIIADRPMASTEVITSOERETIKK 115
Db 54 KGVILPWPENSLGDKTARVYFVALIYMLGVSIIADRPMSIEVITSOERETIKK 113
116 KPNGETSTTIRVNNETVSNLTLMALGSSAPEILSLIEVCGHGFAGDLGPTIVGSA 175
Db 114 KPNGETSTTIRVNNETVSNLTLMALGSSAPEILSLIEVCGHGFAGDLGPTIVGSA 173
176 FNMFIIGICVYVIPGERTKIKHLRVFFITTAANSIFAYITWYILAVSPGVQVWEG 235
Db 174 FNMFIIGICVYVIPGERTKIKHLRVFFITTAANSIFAYITWYILAVSPGVQVWEG 233
Qy 236 LTFEFPVCYLLAVADKRLLEFYKMHKKYKTDKNGIITTEEDHPK---TEMCKM 292
Db 234 LTFEFPVCYLLAVADKRLLEFYKMHKKYKTDKNGIITTEEDHPK---TEMCKM 293
293 NSH---FLDGNLVPYLVKGEVD---ESRREMIIRILDKOKHPEKDLQVLEMANUY 345
Db 294 NSHVDNFDLQALV-LVDEDEDDDEARREARILKELKOKHPEKDLQVLEMANUY 352
Qy 346 HQKSRAFRIQATRLMTGNTLKRAADQARKAVSMHVNMDVVENDPVSFFEQGT 412
Db 353 QOQKSRAFRIQATRLMTGNTLKRAADQARKAVSMHVNMDVVENDPVSFFEQGT 412
Qy 405 YQLENCQAVLTVVRKGGMSKTMVVDYKTEKDSANAGADYFETGTVLTKGGEPOKE 464
Db 413 YQLENCQAVLTVVRKGGMSKTMVVDYKTEKDSANAGADYFETGTVLTKGGEPOKE 472
Qy 465 SVGIIDDDIFEEDHFFVRLSNVRIEEOPEEGMPAIFNSLPUR-AVLASPCVATVTI 523
Db 473 RVGIIDDDIFEEDHFFVRLSNVRIEEOPEEGMPAIFNSLPUR-AVLASPCVATVTI 528
Qy 524 LDDDHAGIFTEECDDTHVSSISGVMEYKVLRTSGARCTVVPRTVEGTAKGGEDFET 583
Db 529 FDDDHAGIFTEECDDTHVSSISGVMEYKVLRTSGARCTVVPRTVEGTAKGGEDFET 588
Qy 584 YGELEFRKNDTV 595
Db 589 YGELEFRKNDTV 599
```

[illegible]

N.Alternate names: Na+/Ca2+ antiporter; Na+/Ca2+ exchanger
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 18-Aug-2000
C:Accession: S28833; S25552
R:Low, W.; Kasir, J.; Rahamimoff, H.
FEBS Lett. 316, 63-67, 1993
A:Title: Cloning of the rat heart Na(+)-Ca(2+) exchanger and its functional expression
A:Reference number: S28833; MUID:93138118; PMID:8422940
A:Accession: S28833
A:Molecule type: mRNA
A:Residues: 1-971 <LOW>
A:Cross-references: EMBL:X68191; NID:957208; PIDN:CAA8273.1; PID:957209
C:Superfamily: human Na+/Ca2+-exchanging protein
C:Keywords: ion transport; membrane protein; phosphoprotein

Query Match 66.0%; Score 2129.5; DB 2; Length 971;
Best Local Similarity 68.6%; Pred. No. 5.8e-155;
Matches 420; Conservative 72; Mismatches 87; Indels 33; Gaps 9;

QY 4 LRLQPLTSALFLHFGVLTFLVLF-----NGLRAAGSGDVSTGONNESCSSGSDCK 55
DB 2 LRLSLPKNVSMGFRVLTVALLFTHVDHITADTAETSGN-----ETTECGSYCK 53
QY 56 EGVILPIYKPNPSSGDKIARYVYFVALIYFGLGVSIIDRFNASIVITISOEREVITIK 115
DB 54 KGVILPIKPEOPSPSGDKIARYVYFVALIYFGLGVSIIDRFNASIVITISOEREVITIK 113
QY 116 KNGESTTTIRVNMETVSNLTLMALGSSAPETLLSLEVGCHGFIAGDLPSRTVGSAA 175
DB 114 KNGESTTTIRVNMETVSNLTLMALGSSAPETLLSLEVGCHGHNFTADLPSRTVGSAA 173
QY 176 FMNFIITIGCVVIRPDGSTRKIKHLRVEFIITAAMSIFAYIMLYMLIAVSPGVQVWEG 235
DB 174 FMNFIITMLCVVYVVDGETGRKIKHLRVEFIITAAMSIFAYIMLYMLIYSSPGVVEWEG 233
QY 236 LTLFFEPYCVLLAVNADKRLLEFYKYMHKKYRTDKHGIILETSGDPKG---IEMDGKM 292
DB 234 LTLFFEPYCVVPAWVAARLLLEFYKYKRYBRAGQRMIIIEHGDPAASKTEIEMDGKV 293
QY 293 NSH---FLDGNLYPLEGKEDV---ESRRERIRILKDKOKHPEDLDQVLEMANIYALS 345
DB 294 NSHVNDFLDGALV-LEVERDODDDEARREMARILKELOKHHPDEISQLEELANYOVL 352
QY 346 HQKSRAPYRIQATPMATGAGNLIKKAHAEOAKKASSEKVTDEPE-DFIASKYFDPDS 404
DB 353 QOKSRAPYRIQATLMTGAGNLIKKAHAADAKKAVSHVEVMNDVENDAVSKYFEDGT 412
QY 405 YQCLNCGAVLLTVVRKGDMSKTYVDYKTEDGSANAGADYEFTGTVLAKPGETOKF 464
DB 413 YQCLNCGVALLTIRRGDGLNTVFDFRTEDGTANAGSDYEFTEGVIRPKPGTQKEI 472
QY 465 SVGIITDDIIFEDDEHFYRLSNVRIEEOQPEGMALFNSLPLR-AVLASPCVATYTI 523
DB 473 RGVIIITDDIIFEDDENFLVHLSNVRSSEVSEDG---FLDSNHSALACLSPTATYTI 528
QY 524 LDDHAGIYFTFPCDRIHVSSEIGVMEVVKLRTSGARGTVIYPPFRVEGTAKGGGDFEDT 583
DB 529 FDDHAGIYFTFPEPRTYHVSSEIGIWEVKVLTISARGNVITIPKTIESTANGGGEDEDT 588
QY 584 YGELEFKNDETV 595
DB 589 GGELEFONDETV 600

RESULT 10
AS4139

A:Cross-references: EMBL:Z70312; PIDN:CAA94387.1; GSPDB:GN00022; CESP:ZC168.1

A:Experimental source: clone ZC168

C:Genetics:

A:Gene: CESP:ZC168.1

A:Map position: 4

A:Introns: 38/1, 177/3; 346/1; 365/1; 369/3; 414/3; 455/3; 692/3; 743/2

Query Match 19.6% Score 633.5; DB 2; Length 807;

Best Local Similarity 29.1%; Pred. No. 2,6e-40;

Matches 174; Conservative 96; Mismatches 174; Indels 153; Gaps 18;

```

47 SCGSSDCEGVILPIMYENPSLGDRIKIRVIVFALYIMFVSIIDRFMASIEVIT 106
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2 SSANLTCNGIL-----PALETPNALIYLANGLFCFGLIADIFCSEIGIT 54
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
107 SQREVTIKKPKNGETSTT-----IRVNETVSNLTALGSSAPEILLIEY 155
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
55 SATKKYKKKKKKGOLVAKKEDEDEIDQYDVRITMPTVANLTALGSSAPEILLIEI 114
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
156 CGHGFAGLGPSTIVGSAFNMFTIIGCVYIIPDGEIRIKHLVFFETAMSTFAYI 215
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
115 VNGFGAGDGPCTIVGSAFNLFCISALCFVAV-CTQTKRIELVNFVTAFFGFAYI 173
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
216 WLYMILAVSPGVQVQWEGILTFEPFVCLAMVADKRLFFKYMKKYRTD----- 268
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
174 WFLVLIIVITPNVDVMEAILTLFLLVVSVAVDQI-----WKKKSSDLQLELEM 228
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
269 -KRRGIITEGDHPKGIEMCKMNSHFL-----DGNLVPLEGEYDESR----- 314
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
229 AHDGKV-----DDQPEKLSDEIKMANSNLKNEENDVIYDAPSVYVWRMRSISHY 284
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
315 -----EMIRILDKQKHPKDLQLEVMANYALSHQ 348
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
285 PLSDEDOAKILARYSRKMSHDRLYRIRAIQOLSSMRKSEEEVLEKMEQESDSAS 344
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
349 KSRAF-----YRIQAT-----RMATGANTLKHAEOAK-----KASSM 383
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
345 RRKEFEFSARVYVDATDETYSKIERKGMESKFTVSATVYNGLAKKOLNLFKSETL 404
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
384 -----SEVH-----TDEPEFISKVFDPDPC--SYQCLENGC 412
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
405 QFNPEGLHTISLIQLIANAMRPNDVYVHLKIQDVED--SKICGACVAVAHVKNAG 462
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
413 AVLLTVARRKGMSTMYDYKTEGDSANAGADY-EFTGCTVVLKKGTEKESVGIID 471
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
463 FRSFSTTRKGGKLLKFLQVHYETEDYAKGGDDYVAKDILFEGQETEKYIDIVID 522
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
472 DIFEDEHFFVRLSNVRIEEOPEEGMPAIFNSLPRAVLASPCVATVITLDDH 528
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
523 KMDKEARFIEL--LKVD-----PCVSICTRRKATITITISDN 560
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 13

T00424

Probable Na⁺/Ca²⁺ antiporter [imported] - Arabidopsis thaliana

N:Alternate names: hypothetical protein T30B22.10

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #extl_change 16-Feb-2001

C:Accession: T00424; C84917

R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Masc

submitted to the EMBL Data Library, October 1998

A:Description: Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence.

A:Reference number: Z14149

A:Accession: T00424

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-538 <ROU>

A:Cross-references: EMBL:AC002535; NID:g3529657; PID:g3522931

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Motilal, K.S.; Cronin, L.A.; Shen, M.; Van den, S.E.; Umayam, L.; Tallon, L.

enuss, D.; Meriman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: AB4420; MID:20083487; PMID:10617197

A:Accession: C84917

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-538 <STO>

A:Cross-references: GB:AE002093; NID:g3529331; PIDN:AAC62871.1; GSPDB:GN00139

C:Genetics:

A:Gene: AT2g47600; T30B22.10

A:Map position: 2

A:Introns: 131/1; 189/3; 229/2; 287/1; 333/1; 397/1; 440/2

Query Match 11.2% Score 362.5; DB 2; Length 538;

Best Local Similarity 31.3%; Pred. No. 9.3e-20;

Matches 91; Conservative 61; Mismatches 96; Indels 43; Gaps 9;

```

64 YPENPSLGDRIKIRVIVFALYIMFVSIIDRFMASIEVITSOEREVTIKKPKNGETST 123
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
29 FPGENTLSQGL-RGVLYFLGLAYCFGLSAITRAFESKMEVNVKHSKVVITDIPTRAEV 87
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
124 TTI-RVWNETVSNLTALGSSAPEILLIEY---CGHGFAGDGPSTIVGSAFNMFT 179
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
88 IYKKYWNFTIADISLAFSTSPQISLATIDAIRNGERY-AGGLGPTLVGSAAFDLR 146
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
180 IIGICVYVIPDGEIRIKHLVFFETAMSTFAYIWLILAVFSPGVQWEGILTLF 239
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
147 PNAVCVYVPKAGELKISDGLVYELVNSFWAYIMLYITLLEWSPNVTTLLEALLTVL 206
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
240 FFPVCLAMVADKRLFFKYMKKYRTDKHRIITETEGDHPKGIEMCKMNSHFLDG 299
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
207 QYGLLVVHVAQDKR---WFLS-----LPMRSRQDRE----- 236
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
300 NLVPLEGEYDESR---REMIRILDKQKHPKDLQLEVMANYALSH 346
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
237 EWPV---EEDITSKDDNDVHDVSDAQAQDAVESGRNIVDIFSHSANN 284
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Query Match 6.4% Score 205; DB 2; Length 1014;

Best Local Similarity 23.6%; Pred. No. 2.7e-07;

Matches 105; Conservative 65; Mismatches 161; Indels 114; Gaps 19;

```

77 VIYFVALIYMFVGSIIADR-FMASIEVITSOEREVTIKKPKNGETSTTIRVWNETVSN 135
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
451 VVHIFGMLYFVALIYDCDEYFVPAAGVITDK-----LQI-SEVYAG 492
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
136 LTLALGSSAPEILLIEYCGHGFIA-GDLGPTIVGSAFNMFTIIGICVYVIPDGET 194
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
493 ATFMAGGSAPELFTSLIGI---FISHSNVIGITIGVAFNILEVIGCALF-----S 543
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
195 RKIKHLRVFPTTAMSFATIMLY-----MILAVSPGVQWEGILTLFFFPVCL-LA 248
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
544 RETLNL-----TWMPLEFRDITFIYIDMLMLLFFPDSLIVWMSLLLLALVALVFTMK 597
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
249 WVADKRLFFKYMKKR-----YRTDKHRIITETEGDHPKGIEMCKMNSHFLDGNLV 302
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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